



#7

1

SEQUENCE LISTING

<110> CHAMBER, PIERRE
METZGER, DANIEL

<120> TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
MEDIATED BY MODIFIED CRE-ER

<130> 065691/0222

<140> 09/853,033

<141> 2001-05-11

<150> FR 00/12570

<151> 2000-10-03

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<170> PatentIn Ver. 2.1

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<211> 1788

<212> DNA

<213> Homo sapiens

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<222> (1)..(1788)

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Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys	
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gcg gcc gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc ccc tac	240
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Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala	
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Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys	
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Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn	
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Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro	
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Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser	
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acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg gac	1440
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Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
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<210> 3

<211> 1983

<212> DNA

<213> Artificial sequence

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<222> (1)..(1983)

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<223> Description of Artificial Sequence: Chimeric sequence
Homosapiens-Bacteriophage P1

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Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg	
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ccc	gca	gaa	cct	gaa	gat	gtt	cgc	gat	tat	ctt	cta	tat	ctt	cag	gcg	240
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gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt	384
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gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432
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Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	
180 185 190	
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Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly	
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Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp	
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260 265 270	
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T03030" E0E5350

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cgc Arg	ctg Leu	ctg Leu	gaa Glu 340	gat Asp	ggc Gly	gat Asp	ctc Leu	gag Glu	cca Pro	tct Ser	gct Ala	gga Gly	gac Asp 350	atg Met	aga Arg	1056
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Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
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Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
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Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
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Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
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<211>	1983
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<223> Description of Artificial Sequence: Chimeric sequence
Homosapiens-Bacteriophage P1

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Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

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Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

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Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

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gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat 480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

ctg	gca	ttt	ctg	ggg	att	gct	tat	aac	acc	ctg	tta	cgt	ata	gcc	gaa	528
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	
				165					170					175		

att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga 576
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

atg Met	tta Leu	atc Ile 195	cat His	att Ile	ggc Gly	aga Arg	acg Thr 200	aaa Lys	acg Thr	ctg Leu	gtt Val	agc Ser 205	acc Thr	gca Ala	ggt Gly	624
gta Val	gag Glu 210	aag Lys	gca Ala	ctt Leu	agc Ser 215	ctg Leu	ggg Gly	gta Val	act Thr	aaa Lys 220	ctg Leu	gtc Val	gag Glu	cga Arg	tgg Trp	672
att Ile 225	tcc Ser	gtc Val	tct Ser	ggt Gly	gta Val 230	gct Ala	gat Asp	gat Asp	ccg Pro 235	aat Asn	aac Asn	tac Tyr	ctg Leu	ttt Phe	tgc Cys 240	720
cgg Arg	gtc Val	aga Arg	aaa Lys	aat Asn 245	ggt Gly	gtt Val	gcc Ala	gcg Ala	cca Pro 250	tct Ser	gcc Ala	acc Thr	agc Ser	cag Gln 255	cta Leu	768
tca Ser	act Thr	cgc Arg 260	gcc Ala	ctg Leu	gaa Glu	ggg Gly	att Ile 265	ttt Phe	gaa Glu	gca Ala	act Thr	cat His 270	cga Arg	ttg Leu	att Ile	816
tac Tyr	ggc Gly 275	gct Ala	aag Lys	gat Asp	gac Asp	tct Ser	ggt Gly 280	cag Gln	aga Arg	tac Tyr	ctg Leu	gcc Ala 285	tgg Trp	tct Ser	gga Gly	864
cac His	agt Ser 290	gcc Ala	cgt Arg	gtc Val	gga Gly	gcc Ala 295	gcg Ala	cga Arg	gat Asp	atg Met 300	gcc Ala	cgc Arg	gct Ala	gga Gly	gtt Val	912
tca Ser 305	ata Ile	ccg Pro	gag Glu	atc Ile	atg Met 310	caa Gln	gct Ala	ggc Gly	ggc Gly	tgg Trp 315	acc Thr	aat Asn	gta Val	aat Asn	att Ile 320	960
gtc Val	atg Met	aac Asn	tat Tyr	atc Ile 325	cgt Arg	aac Asn	ctg Leu	gat Asp	agt Ser 330	gaa Glu	aca Thr	ggg Gly	gca Ala	atg Met 335	gtg Val	1008
cgc Arg	ctg Leu	ctg Leu	gaa Glu 340	gat Asp	ggc Gly	gat Asp	ctc Leu	gag Glu 345	cca Pro	tct Ser	gct Ala	gga Gly	gac Asp 350	atg Met	aga Arg	1056
gct Ala	gcc Ala	aac Asn 355	ctt Leu	tgg Trp	cca Pro	agc Ser	ccg Pro 360	ctc Leu	atg Met	atc Ile	aaa Lys 365	cgc Arg	tct Ser	aag Lys	aag Lys	1104
aac Asn	agc Ser 370	ctg Leu	gcc Ala	ttg Leu	tcc Ser	ctg Leu 375	acg Thr	gcc Ala	gac Asp	cag Gln 380	atg Met	gtc Val	agt Ser	gcc Ala	ttg Leu	1152
ttg Leu 385	gat Asp	gct Ala	gag Glu	ccc Pro 390	ccc Pro	ata Ile	ctc Leu	tat Tyr	tcc Ser	gag Glu 395	tat Tyr	gat Asp	cct Pro	acc Thr	aga Arg 400	1200
ccc Pro	ttc Phe	agt Ser	gaa Glu 405	gct Ala	tcg Ser	atg Met	atg Met	ggc Gly	tta Leu 410	ctg Leu	acc Thr	aac Asn	ctg Leu	gca Ala 415	gac Asp	1248

agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt	1296
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
			420					425					430			
gtg	gat	ttg	acc	ctc	cat	gat	cag	gtc	cac	ctt	cta	gaa	tgt	gcc	tgg	1344
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
		435					440					445				
cta	gag	atc	ctg	atg	att	ggg	ctc	gtc	tgg	cgc	tcc	atg	gag	cac	cca	1392
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
		450				455					460					
gtg	aag	cta	ctg	ttt	gct	cct	aac	ttg	ctc	ttg	gac	agg	aac	cag	gga	1440
Val	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
	465				470					475					480	
aaa	tgt	gta	gag	ggc	atg	gtg	gag	atc	ttc	gac	atg	ctg	ctg	gct	aca	1488
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	
			485						490					495		
tca	tct	cgg	ttc	cgc	atg	atg	aat	ctg	cag	gga	gag	gag	ttt	gtg	tgc	1536
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	
			500					505					510			
ctc	aaa	tct	att	att	ttg	ctt	aat	tct	gga	gtg	tac	aca	ttt	ctg	tcc	1584
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser	
		515					520					525				
agc	acc	ctg	aag	tct	ctg	gaa	gag	aag	gac	cat	atc	cac	cga	gtc	ctg	1632
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu	
		530				535					540					
gac	aag	atc	aca	gac	act	ttg	atc	cac	ctg	atg	gcc	aag	gca	ggc	ctg	1680
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu	
		545			550					555					560	
acc	ctg	cag	cag	cag	cac	cag	cgg	ctg	gcc	cag	ctc	ctc	ctc	atc	ctc	1728
Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu	
			565					570						575		
tcc	cac	atc	agg	cac	atg	agt	aac	aaa	ggc	atg	gag	cat	ctg	tac	agc	1776
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser	
			580					585					590			
atg	aag	tgc	aag	aac	gtg	gtg	ccc	ctc	tat	gac	ctg	ctg	ctg	gag	gcg	1824
Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala	
		595					600					605				
gcg	gac	gcc	cac	cgc	cta	cat	gcg	ccc	act	agc	cgt	gga	ggg	gca	tcc	1872
Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly				

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

cct gcc aca gct tga 1983
 Pro Ala Thr Ala
 660

<210> 6
 <211> 660
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of Artificial Sequence: Chimeric sequence
 Homosapiens-Bacteriophage P1

<400> 6
 Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15
 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30
 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80
 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95
 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110
 Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125
 Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140
 Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160
 Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175
 Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190
 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

005003 000004
 000000 000000

Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	210	215	220	
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	225	230	235	240
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	245	250	255	
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	260	265	270	
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	275	280	285	
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	290	295	300	
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	305	310	315	320
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	325	330	335	
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	340	345	350	
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	355	360	365	
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	370	375	380	
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	385	390	395	400
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	405	410	415	
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	420	425	430	
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	435	440	445	
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	450	455	460	
Val	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	465	470	475	480
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	485	490	495	
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	500	505	510	

T08080"EE0E9860

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<210> 7
<211> 1983
<212> DNA
<213> Artificial sequence
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<220>
<223> Description of Artificial Sequence: Chimeric sequence
Homosapiens-Bacteriophage P1

<400> 7																
atg	tcc	aat	tta	ctg	acc	gta	cac	caa	aat	ttg	cct	gca	tta	ccg	gtc	48
Met	Ser	Asn	Leu	Leu	Thr	Val	His	Gln	Asn	Leu	Pro	Ala	Leu	Pro	Val	
1		5			10					15						
gat	gca	acg	agt	gat	gag	gtt	cgc	aag	aac	ctg	atg	gac	atg	ttc	agg	96
Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg	
			20		25				30							
gat	cgc	cag	gcg	ttt	tct	gag	cat	acc	tgg	aaa	atg	ctt	ctg	tcc	gtt	144
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val	
		35			40				45							

tgc Cys	cgg Arg 50	tcg Ser	tgg Trp	gcg Ala	gca Ala	tgg Trp 55	tgc Cys	aag Lys	ttg Leu	aat Asn	aac Asn 60	cgg Arg	aaa Lys	tgg Trp	ttt Phe	192
ccc Pro 65	gca Ala	gaa Glu	cct Pro	gaa Glu	gat Asp 70	gtt Val	cgc Arg	gat Asp	tat Tyr	ctt Leu 75	cta Leu	tat Tyr	ctt Leu	cag Gln	gcg Ala 80	240
cgc Arg	ggg Gly	ctg Leu	gca Ala	gta Val 85	aaa Lys	act Thr	atc Ile	cag Gln	caa Gln 90	cat His	ttg Leu	ggc Gly	cag Gln	cta Leu 95	aac Asn	288
atg Met	ctt Leu	cat His	cgt Arg 100	cgg Arg	tcc Ser	ggg Gly	ctg Leu	cca Pro 105	cga Arg	cca Pro	agt Ser	gac Asp	agc Ser 110	aat Asn	gct Ala	336
gtt Val	tca Ser 115	ctg Leu	gtt Val	atg Met	cgg Arg	cgg Arg	atc Ile 120	cga Arg	aaa Lys	gaa Glu	aac Asn	gtt Val 125	gat Asp	gcc Ala	ggg Gly	384
gaa Glu 130	cgt Arg	gca Ala	aaa Lys	cag Gln	gct Ala	cta Leu 135	gcg Ala	ttc Phe	gaa Glu	cgc Arg	act Thr 140	gat Asp	ttc Phe	gac Asp	cag Gln	432
gtt Val 145	cgt Arg	tca Ser	ctc Leu	atg Met	gaa Glu 150	aat Asn	agc Ser	gat Asp	cgc Arg	tgc Cys 155	cag Gln	gat Asp	ata Ile	cgt Arg	aat Asn 160	480
ctg Leu	gca Ala	ttt Phe	ctg Leu	ggg Gly 165	att Ile	gct Ala	tat Tyr	aac Asn	acc Thr 170	ctg Leu	tta Leu	cgt Arg	ata Ile	gcc Ala 175	gaa Glu	528
att Ile	gcc Ala	agg Arg	atc Ile 180	agg Arg	gtt Val	aaa Lys	gat Asp 185	atc Ile	tca Ser	cgt Arg	act Thr	gac Asp	ggg Gly 190	ggg Gly	aga Arg	576
atg Met	tta Leu 195	atc Ile	cat His	att Ile	ggc Gly	aga Arg	acg Thr 200	aaa Lys	acg Thr	ctg Leu	gtt Val	agc Ser 205	acc Thr	gca Ala	ggg Gly	624
gta Val 210	gag Glu	aag Lys	gca Ala	ctt Leu	agc Ser	ctg Leu 215	ggg Gly	gta Val	act Thr	aaa Lys	ctg Leu 220	gtc Val	gag Glu	cga Arg	tgg Trp	672
att Ile 225	tcc Ser	gtc Val	tct Ser	ggg Gly	gta Val 230	gct Ala	gat Asp	gat Asp	cgc Pro	aat Asn 235	aac Asn	tac Tyr	ctg Leu	ttt Phe	tgc Cys 240	720
cgg Arg	gtc Val	aga Arg	aaa Lys	aat Asn 245	ggg Gly	gtt Val	gcc Ala	gcg Ala	cca Pro 250	tct Ser	gcc Ala	acc Thr	agc Ser	cag Gln 255	cta Leu	768
tca Ser	act Thr	cgc Arg	gcc Ala	ctg Leu	gaa Glu	ggg Gly	att Ile	ttt Phe 265	gaa Glu	gca Ala	act Thr	cat His	cga Arg	ttg Leu	att Ile	816

tac Tyr	ggc Gly	gct Ala 275	aag Lys	gat Asp	gac Asp	tct Ser	ggt Gly 280	cag Gln	aga Arg	tac Tyr	ctg Leu	gcc Ala 285	tgg Trp	tct Ser	gga Gly	864
cac His	agt Ser 290	gcc Ala	cgt Arg	gtc Val	gga Gly	gcc Ala 295	gcg Ala	cga Arg	gat Asp	atg Met	gcc Ala 300	cgc Arg	gct Ala	gga Gly	gtt Val	912
tca Ser 305	ata Ile	ccg Pro	gag Glu	atc Ile	atg Met 310	caa Gln	gct Ala	ggt Gly	ggc Gly	tgg Trp 315	acc Thr	aat Asn	gta Val	aat Asn	att Ile 320	960
gtc Val	atg Met	aac Asn	tat Tyr	atc Ile 325	cgt Arg	aac Asn	ctg Leu	gat Asp	agt Ser 330	gaa Glu	aca Thr	ggg Gly	gca Ala	atg Met 335	gtg Val	1008
cgc Arg	ctg Leu	ctg Leu	gaa Glu 340	gat Asp	ggc Gly	gat Asp	ctc Leu	gag Glu	cca Pro	tct Ser	gct Ala	gga Gly 350	gac Asp	atg Met	aga Arg	1056
gct Ala	gcc Ala	aac Asn 355	ctt Leu	tgg Trp	cca Pro	agc Ser	ccg Pro 360	ctc Leu	atg Met	atc Ile	aaa Lys 365	cgc Arg	tct Ser	aag Lys	aag Lys	1104
aac Asn 370	agc Ser	ctg Leu	gcc Ala	ttg Leu	tcc Ser	ctg Leu 375	acg Thr	gcc Ala	gac Asp	cag Gln	atg Met 380	gtc Val	agt Ser	gcc Ala	ttg Leu	1152
ttg Leu 385	gat Asp	gct Ala	gag Glu	ccc Pro	ccc Pro 390	ata Ile	ctc Leu	tat Tyr	tcc Ser	gag Glu 395	tat Tyr	gat Asp	cct Pro	acc Thr	aga Arg 400	1200
ccc Pro	ttc Phe	agt Ser	gaa Glu	gct Ala 405	tcg Ser	atg Met	atg Met	ggc Gly	tta Leu 410	ctg Leu	acc Thr	aac Asn	ctg Leu	gca Ala 415	gac Asp	1248
agg Arg	gag Glu	ctg Leu	gtt Val 420	cac His	atg Met	atc Ile	aac Asn	tgg Trp 425	gcg Ala	aag Lys	agg Arg	gtg Val	cca Pro 430	ggc Gly	ttt Phe	1296
gtg Val	gat Asp	ttg Leu 435	acc Thr	ctc Leu	cat His	gat Asp	cag Gln	gtc Val	cac His	ctt Leu	cta Leu	gaa Glu 445	tgt Cys	gcc Ala	tgg Trp	1344
cta Leu 450	gag Glu	atc Ile	ctg Leu	atg Met	att Ile	ggt Gly 455	ctc Leu	gtc Val	tgg Trp	cgc Arg	tcc Ser 460	atg Met	gag Glu	cac His	cca Pro	1392
ggg Gly 465	aag Lys	cta Leu	ctg Leu	ttt Phe	gct Ala 470	cct Pro	aac Asn	ttg Leu	ctc Leu	ttg Leu 475	gac Asp	agg Arg	aac Asn	cag Gln	gga Gly 480	1440
aaa Lys	tgt Cys	gta Val	gag Glu	ggc Gly 485	atg Met	gtg Val	gag Glu	atc Ile	ttc Phe 490	gac Asp	atg Met	ctg Leu	ctg Leu	gct Ala	aca Thr	1488

tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc 1536
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
 500 505 510

ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc 1584
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
 515 520 525

agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg 1632
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
 530 535 540

gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg 1680
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
 545 550 555 560 565

acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc 1728
 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
 565 570 575

tcc cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc 1776
 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser
 580 585 590

atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg 1824
 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala
 595 600 605

gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca 1920
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

cct gcc aca gct tga 1983
 Pro Ala Thr Ala
 660

<210> 8

<211> 660

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Chimeric sequence
 Homosapiens-Bacteriophage P1

<400> 8

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg	
			20					25					30			
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val	
			35					40					45			
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe	
			50					55					60			
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala	
			65					70					75		80	
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn	
			85					90					95			
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala	
			100					105					110			
Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	
			115					120					125			
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	
			130					135					140			
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	
			145					150					155		160	
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	
			165					170					175			
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	
			180					185					190			
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
			195					200					205			
Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
			210					215					220			
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
			225					230					235		240	
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
			245					250					255			
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
			260					265					270			
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
			275					280					285			
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
			290					295					300			
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
			305					310					315		320	

Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val
				325					330					335	
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg
			340					345					350		
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Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr
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Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu
				565					570					575	
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser
			580					585					590		
Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala
		595					600					605			
Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser
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Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
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